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LOCUS AE008898 23880 bp DNA linear BCT 31-JUL-2002

DEFINITION *Salmonella typhimurium* LT2, section 202 of 220 of the complete genome.

ACCESSION AE008898 AE006468

VERSION AE008898.1

KEYWORDS

SOURCE *Salmonella typhimurium* LT2

ORGANISM *Salmonella typhimurium* LT2  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; *Salmonella*.

REFERENCE 1 (bases 1 to 23880)

AUTHORS McClelland, M., Sanderson, K. E., Spieth, J., Clifton, S. W., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F., Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A., Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W., Stoneking, T., Nhan, M., Waterston, R. and Wilson, R. K.

TITLE Complete genome sequence of *Salmonella enterica* serovar Typhimurium LT2

JOURNAL Nature 413 (6858), 852-856 (2001)

MEDLINE 21534948

PUBMED 11677609

REFERENCE 2 (bases 1 to 23880)

AUTHORS The *Salmonella typhimurium* Genome Sequencing Project.

TITLE Direct Submission

JOURNAL Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA

COMMENT COMMENT Supported by NIH grant 5U 01 AI43283

Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; <http://www.tigr.org/softlab/glimmer/glimmer.html> and GeneMark; <http://opal.biology.gatech.edu/GeneMark/>

EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; <http://www.genome.ad.jp/kegg/>, and Pedro Romero and Peter Karp at EcoCyc; <http://ecocyc.PangeaSystems.com/ecocyc/>

The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; [http://kinich.cifn.unam.mx:8850/db/regulondb\\_intro.frameset](http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset)

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

FEATURES

source Location/Qualifiers

1..23880

/organism="Salmonella typhimurium LT2"

/strain="LT2; SGSC 1412; ATCC 700720"

/db\_xref="ATCC:700720"

/db\_xref="taxon:99287"

/note="LT2"

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/gene="malM"

/note="synonym: STM4232"

RBS 107..112

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gene 1715..2600  
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CDS 1728..2600  
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CDS complement(2699..5119)  
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 (827 aa), 94% identity in aa 21 - 826"

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DDELHINPTHSRTLQLLAAGARETLQRYAITFWLLSANPSINRSTLEKESRTVAQRLS
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RBS complement(5131..5136)
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/Note="putative RBS for plsB; RegulonDB:STMS1H004140"
gene 5278..5658
/gene="dgkA"
/Note="synonym: STM4236"
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/gene="dgkA"
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CDS 5290..5658
/gene="dgkA"
/EC_number="2.7.1.107"
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(AAC77012.1); Blastp hit to AAC77012.1 (122 aa), 86%
identity in aa 1 - 121"
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gene 5701..6375
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RegulonDB:STMLTH004657"
protein_bind 5722..5738
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STMS1H000241"
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RegulonDB:STMLTH004657"
protein_bind 5742..5762
/gene="lexA"
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STMS1H000249"
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CDS 5767..6375
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/Note="transcriptional repressor (LexA family); LEXA

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repressor. (SW:LEXA_SALTY)"
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gene 6540..7878
/gene="dinF"
RBS 6540..6545
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/note="putative RBS for dinF; RegulonDB:STMS1H004143"
CDS 6553..7878
/gene="dinF"
/note="induced by UV and mitomycin C; SOS, lexA regulon;
similar to E. coli DNA-damage-inducible protein F
(AAC77014.1); Blastp hit to AAC77014.1 (459 aa), 89%
identity in aa 19 - 457"
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/db_xref="GI:16422796"
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HIVALLTSLPQIQLLADRYLIWQVVLPLVGVWCYLLDGMFIGATRAAEMRNSMAVAAG
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gene 7998..8219
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RBS 7998..8003
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/note="putative RBS for yjbJ; RegulonDB:STMS1H004144"
CDS 8007..8219
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/note="similar to E. coli orf, hypothetical protein
(AAC77015.1); Blastp hit to AAC77015.1 (69 aa), 95%
identity in aa 1 - 69"
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/translation="MMNKDEAGGNWKQFKGKMKEQWGKLTDDMTVIEGKRDQLVGKI
QERYGYQKDQAEKEVVDWETRNNYRW"
gene complement(8318..8843)
/gene="zur"
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CDS complement(8318..8833)
/gene="zur"
/note="Fur family; similar to E. coli putative regulator
(AAC77016.1); Blastp hit to AAC77016.1 (191 aa), 92%

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identity in aa 21 - 191"  
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DHSVLVKKKPR"  
RBS complement(8838..8843)  
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gene 9076..10390  
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CDS 9080..10390  
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VAIVSDYGIAlAKQFVVGEVPSIGVTPKLQKTWLYNYTTSIYNYDSSDWNSSRYRND  
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gene 10478..11476  
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CDS 10478..11476  
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/note="possibly dehydrogenases; nifR3 family; similar to  
E. coli orf, hypothetical protein (AAC77019.1); Blastp hit  
to AAC77019.1 (345 aa), 90% identity in aa 7 - 345"  
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SDRVQNGMFGACLMGNAQLVADCVKAMRDVVSIPVTVKTRIGIDDQDSYAFLCDFIDT  
VSGQGECEMFIIHARKAWLSGLSPKENREIPPLDYPRVYQLKRDFPHLTMSINGGIKS  
LEEAKEHLRHMDGVMVGREAYQNP GILAAVDREIFGADTTDADPVAVVRAMYPIERE  
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gene complement(12061..13052)

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/note="synonym: STM4245"  
complement(12061..13044)  
/gene="qor"  
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AKALGAKLIGTVGSAQKAQRALDAGAWQVINYREESIVERVKEITGGKKVRVVYDSVG  
KDTWEASLDCLQRRGLMVSFGNASGPVTGVNLGILNQKGSYATRPSLQGYITTREEL  
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AGLQRSDLIIVAARPSMGKTTFAMNLCENAMLQDKPVLIFSLEMPGEQIMMRMLASL  
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CDS 14556..15635  
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PLEHKPWGPDFGFQPVMSLTSSLIAVRDHKAGEPVGYGGTWSERDTRLGVVAMGYGD  
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gene 15773..17014  
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-35\_signal /note="synonym: STM4248"  
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 RegulonDB:STMLTH004658"  
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 GGSGALKVGADFLKRYFPDAGVWVSOPWENHIAIFAGAGFEVSTYPWYDDATNGIRF  
 NDLLATLNTLPARSIVLLHPCCHNPTGADLTSPQWDVIEIVKARDLIPFLDIAYQGF  
 GAGMDDDAYVIRAIASAGLPALVSNFSKIFSLYGERVGGLSVVCEDAEIAARVLGQL  
 KATVRRITYSPPCFGAQQVATVLGDEALKAGWLAEDAMNRIISMRQTLVKELKAEM  
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 FAAVM"  
 gene 17190..17914  
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 CDS 17201..17914  
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